

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/866,354DATE: 05/05/98  
TIME: 14:49:33

INPUT SET: S25543.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

ENTERED

## SEQUENCE LISTING

- 1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Fox, Gary M  
6 Jing, Shuqian  
7 Wen, Duanzhi  
8  
9 (ii) TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTORS  
10  
11 (iii) NUMBER OF SEQUENCES: 44  
12  
13 (iv) CORRESPONDENCE ADDRESS:  
14 (A) ADDRESSEE: AMGEN INC  
15 (B) STREET: One Amgen Center Drive  
16 (C) CITY: Thousand Oaks  
17 (D) STATE: CA  
18 (E) COUNTRY: US  
19 (F) ZIP: 91320-1789  
20  
21 (v) COMPUTER READABLE FORM:  
22 (A) MEDIUM TYPE: Floppy disk  
23 (B) COMPUTER: IBM PC compatible  
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
26  
27 (vi) CURRENT APPLICATION DATA:  
28 (A) APPLICATION NUMBER: US 08/866,354  
29 (B) FILING DATE: 30-MAY-1997  
30 (C) CLASSIFICATION:  
31  
32 (vii) PRIOR APPLICATION DATA:  
33 (A) APPLICATION NUMBER: US 08/837,199  
34 (B) FILING DATE: 14-APR-1997  
35  
36 (vii) PRIOR APPLICATION DATA:  
37 (A) APPLICATION NUMBER: US 60/015,907  
38 (B) FILING DATE: 22-APR-1996  
39  
40 (vii) PRIOR APPLICATION DATA:  
41 (A) APPLICATION NUMBER: US 60/017,221  
42 (B) FILING DATE: 09-MAY-1996  
43  
44 (viii) ATTORNEY/AGENT INFORMATION:  
45 (A) NAME: Curry, Daniel R.  
46 (B) REGISTRATION NUMBER: 32,727

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(C) REFERENCE/DOCKET NUMBER: A-401B

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2568 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 540..1934

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
68 AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA      60
69
70 CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG      120
71
72 CTCTCGAAGA TTACCGCATC TATTTTTTTTTT TTCTTTTTTTTT TCTTTTCCTA GCGCAGATAA      180
73
74 AGTGAGCCCG GAAAGGGAAG GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG      240
75
76 TAAATAAACA AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT      300
77
78 CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG AGCTGAGTCG      360
79
80 CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT TCACTGGATG GAGCTGAACT      420
81
82 TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG GGATCGCTGC ACGCTGAGCT CCCTCGGCAA      480
83
84 GACCCAGCGG CGGCTCGGGA TTTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACC      539
85
86 ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC      587
87 Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
88 1 5 10 15
89
90 CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC      635
91 Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
92 20 25 30
93
94 AGT GAT CAG TGC CTG AAG GAG CAG AGC TGC AGC ACC AAG TAC CGC ACG      683
95 Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
96 35 40 45
97
98 CTA AGG CAG TGC GTG GCG GGC AAG GAG ACC AAC TTC AGC CTG GCA TCC      731
99 L u Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
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100	50	55	60	
101				
102	GGC CTG GAG GCC AAG GAT GAG TGC CGC AGC GCC ATG GAG GCC CTG AAG	779		
103	Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys			
104	65 70 75 80			
105				
106	CAG AAG TCG CTC TAC AAC TGC CGC TGC AAG CGG GGT ATG AAG AAG GAG	827		
107	Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu			
108	85 90 95			
109				
110	AAG AAC TGC CTG CGC ATT TAC TGG AGC ATG TAC CAG AGC CTG CAG GGA	875		
111	Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly			
112	100 105 110			
113				
114	AAT GAT CTG CTG GAG GAT TCC CCA TAT GAA CCA GTT AAC AGC AGA TTG	923		
115	Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu			
116	115 120 125			
117				
118	TCA GAT ATA TTC CGG GTG GTC CCA TTC ATA TCA GAT GTT TTT CAG CAA	971		
119	Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln			
120	130 135 140			
121				
122	GTG GAG CAC ATT CCC AAA GGG AAC AAC TGC CTG GAT GCA GCG AAG GCC	1019		
123	Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala			
124	145 150 155 160			
125				
126	TGC AAC CTC GAC GAC ATT TGC AAG AAG TAC AGG TCG GCG TAC ATC ACC	1067		
127	Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr			
128	165 170 175			
129				
130	CCG TGC ACC ACC AGC GTG TCC AAC GAT GTC TGC AAC CGC CGC AAG TGC	1115		
131	Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys			
132	180 185 190			
133				
134	CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG GTC CCG GCC AAG CAC AGC	1163		
135	His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser			
136	195 200 205			
137				
138	TAC GGA ATG CTC TTC TGC TCC TGC CGG GAC ATC GCC TGC ACA GAG CGG	1211		
139	Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg			
140	210 215 220			
141				
142	AGG CGA CAG ACC ATC GTG CCT GTG TGC TCC TAT GAA GAG AGG GAG AAG	1259		
143	Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys			
144	225 230 235 240			
145				
146	CCC AAC TGT TTG AAT TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC	1307		
147	Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys			
148	245 250 255			
149				
150	AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA AGG	1355		
151	Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg			
152	260 265 270			

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153																	
154	TCT	GTC	AGC	AGC	TGT	CTA	AAG	GAA	AAC	TAC	GCT	GAC	TGC	CTC	CTC	GCC	1403
155	Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala	
156			275					280					285				
157																	
158	TAC	TCG	GGG	CTT	ATT	GGC	ACA	GTC	ATG	ACC	CCC	AAC	TAC	ATA	GAC	TCC	1451
159	Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser	
160		290				295					300						
161																	
162	AGT	AGC	CTC	AGT	GTG	GCC	CCA	TGG	TGT	GAC	TGC	AGC	AAC	AGT	GGG	AAC	1499
163	Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn	
164	305					310					315					320	
165																	
166	GAC	CTA	GAA	GAG	TGC	TTG	AAA	TTT	TTG	AAT	TTC	TTC	AAG	GAC	AAT	ACA	1547
167	Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr	
168					325					330					335		
169																	
170	TGT	CTT	AAA	AAT	GCA	ATT	CAA	GCC	TTT	GGC	AAT	GGC	TCC	GAT	GTG	ACC	1595
171	Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr	
172				340					345					350			
173																	
174	GTG	TGG	CAG	CCA	GCC	TTC	CCA	GTA	CAG	ACC	ACC	ACT	GCC	ACT	ACC	ACC	1643
175	Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	
176			355					360					365				
177																	
178	ACT	GCC	CTC	CGG	GTT	AAG	AAC	AAG	CCC	CTG	GGG	CCA	GCA	GGG	TCT	GAG	1691
179	Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu	
180		370					375					380					
181																	
182	AAT	GAA	ATT	CCC	ACT	CAT	GTT	TTG	CCA	CCG	TGT	GCA	AAT	TTA	CAG	GCA	1739
183	Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala	
184	385					390					395					400	
185																	
186	CAG	AAG	CTG	AAA	TCC	AAT	GTG	TCG	GGC	AAT	ACA	CAC	CTC	TGT	ATT	TCC	1787
187	Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Asn	Thr	His	Leu	Cys	Ile	Ser	
188					405					410					415		
189																	
190	AAT	GGT	AAT	TAT	GAA	AAA	GAA	GGT	CTC	GGT	GCT	TCC	AGC	CAC	ATA	ACC	1835
191	Asn	Gly	Asn	Tyr	Glu	Lys	Glu	Gly	Leu	Gly	Ala	Ser	Ser	His	Ile	Thr	
192				4													

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206 GTTATCTGTT TCCTGTTCTC TTGTATAGCT GAAATTCCAG TTTAGGAGCT CAGTTGAGAA 2044
207
208 ACAGTTCCAT TCAACTGGAA CATTMTTTTTTT TTTNCCTTTT AAGAAAGCTT CTTGTGATCC 2104
209
210 TTNGGGGCTT CTGTGAAAAA CCTGATGCAG TGCTCCATCC AAACTCAGAA GGCTTTGGGA 2164
211
212 TATGCTGTAT TTAAAGGGA CAGTTTGTA CTTGGGCTGT AAAGCAAACCT GGGGCTGTGT 2224
213
214 TTTCGATGAT GATGATNATC ATGATNATGA TNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 2284
215
216 NNNNNNNNNN GATTTTAACA GTTTTACTTC TGGCCTTTCC TAGCTAGAGA AGGAGTTAAT 2344
217
218 ATTTCTAAGG TAACTCCCAT ATCTCCTTTA ATGACATTGA TTTCTAATGA TATAAATTTT 2404
219
220 AGCCTACATT GATGCCAAGC TTTTTTGCCA CAAAGAAGAT TCTTACCAAG AGTGGGCTTT 2464
221
222 GTGGAAACAG CTGGTACTGA TGTTACCTT TATATATGTA CTAGCATTTT CCACGCTGAT 2524
223
224 GTTTATGTAC TGTAACAGT TCTGCACTCT TGTACAAAAG AAAA 2568
225
226

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

237
238 Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
239 1 5 10 15
240
241 Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
242 20 25 30
243
244 Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
245 35 40 45
246
247 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
248 50 55 60
249
250 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
251 65 70 75 80
252
253 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
254 85 90 95
255
256 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
257 100 105 110
258

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/866,354**

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Line	Error	Original Text
895	Stop Codon at end of sequence removed - no error	
1841	Stop Codon at end of sequence removed - no error	
2235	Stop Codon at end of sequence removed - no error	
2356	Stop Codon at end of sequence removed - no error	